

```

RESULT      1
Y92322
ID   Y92322 standard; Protein; 1145 AA.
XX
AC   Y92322;
XX
DT   10-AUG-2000   (first entry)
XX
DE   Human alpha-2-delta-B calcium channel subunit polypeptide.
XX
KW   alpha-2-delta-B; calcium channel subunit; 3p21.3; gabapentin; cytostatic;
KW   anticonvulsant; antimigrane; antiparkinsonian; antidepressant.
XX
OS   Homo sapiens.
XX
PN   WO200020450-A2.
XX
PD   13-APR-2000.
XX
PF   07-OCT-1999;   99WO-US23519.
XX
PR   07-OCT-1998;   98US-0103322.
PR   30-OCT-1998;   98US-0106473.
PR   29-DEC-1998;   98US-0114088.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Johns MA,   Moldover B,   Offord JD;
XX
DR   WPI; 2000-303744/26.
DR   N-PSDB; A09255.
XX
PT   New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT   proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT   anxiety, multiple sclerosis or cancer
XX
PS   Example 1; Page 62-63; 88pp; English.
XX
CC   The alpha-2-delta-B gene encodes a calcium channel subunit polypeptide.
CC   The gene has been mapped to chromosome 3p21.3. This gene and the related
CC   alpha-2-delta-C and -D genes are useful for protecting mammalian cells
CC   from abnormal calcium flux by introducing expression vectors containing
CC   the respective gene into mammalian cells. The antisense genes are also
CC   useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC   is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC   Therefore, alpha-delta-2 proteins may also be targeted to treat
CC   seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
CC   pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC   multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC   addiction syndromes, mood, depression or cancer.
XX
SQ   Sequence      1145 AA;

```

```

Query Match          100.0%; Score 6089; DB 21; Length 1145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAVPARTCGASRPGPARTARPWPGCGPHPGPGTRRPTSGPPRPLWLLLPLLLPLLAAPGAS 60
        |||
Db      1 mavpartcgasrpgpartarpwpgcgphpgpgtrrptsgpprplwlllplllpllaapgas 60

Qy     61 AYSFPQQHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFQENEPQKLVEKVA 120
        |||
Db     61 aysfpqqhtmqhwarreleqvvgvmrifggvqqlreiykdnrnlfevqenepqklvekva 120

Qy    121 GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER 180
        |||
Db    121 gdieslldrkvqalkrladaaenfqkahrwqdnikeedivyydakadaelddpesedver 180

Qy    181 GSKASTLRDLFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTALENVFMENRR 240

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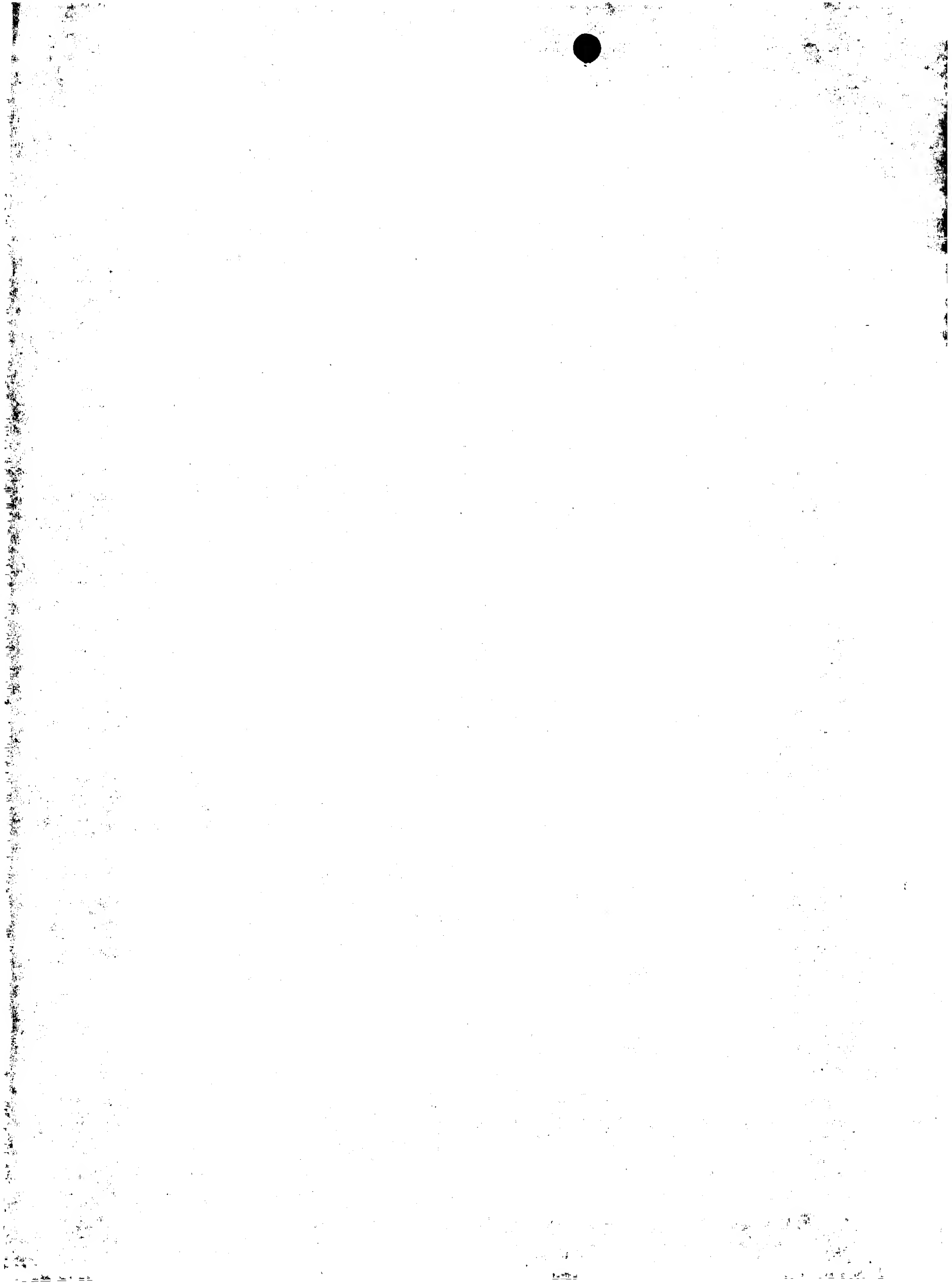
```

Db      181  |||||gskastlrldfiedpnfknkvnsyaavqiptdiykgstvilnelnwtealenvfmenrr 240
Qy      241  QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG 300
Db      241  |||||qdptllwqvfgsatgvtryypatpwrapkkidlydvrppwyiqgasspkdmviivdvsg 300
Qy      301  SVSGLTLKLMKTSVCEMLDLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV 360
Db      301  |||||svsgltlklmktsvcemldtlsdddyvnvasfnekaqpvscthllvqanvrnkkvfkeav 360
Qy      361  QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEKYNWPNRT 420
Db      361  |||||qgmvakgttgykagfeyafdqlqnsnitrancnkmimmftdggedrvqdvfekynwpnrt 420
Qy      421  VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA 480
Db      421  |||||vrvftfsvgqhnydvtplqwmacankgyffeipsigairintqeyldvlgrpmvlagkea 480
Qy      481  KQVQWTVNYEDALGLGLVVTGTLFVFNLTQDGPGEKKNQLILGVMGIDVALNDIKRLTPN 540
Db      481  |||||kqvqwtvnyedalglglvvtgtlpvfnltqdgpgkekknqlilgvmgidvalndikrltpn 540
Qy      541  YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSIDGN 600
Db      541  |||||ytlgangyvfaidlngyvllhpnlpqttnfrepvtldfldaeledenkeeirrsidgn 600
Qy      601  KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLVLPYSTFYLANLSDQILQV 660
Db      601  |||||kghkqirtlvkslderyidevtrnytwvpirstnysglvlppystfylqanlsdqilqv 660
Qy      661  KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTEFLKNFIELMEKVTPDSKQCNNFL 720
Db      661  |||||kyfefllpssfeseghvfiapreyckdlnasdnnteflknfielmekvtpdskqcnnfl 720
Qy      721  HNLILDTGITQQLVERVWRDQDLNTYSLAVFAATDGGITRVFPNKAEDWTENPEPFNA 780
Db      721  |||||hnlildtgitqqlvervwrddqdlntysslavfaatdggitrvfnpkaaedwtenpepfna 780
Qy      781  SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGVKLD 840
Db      781  |||||sfyrrsldnhgyvfkpphqdallrplelendtvgilvstavelslgrrtlrapvvgvkld 840
Qy      841  LEAWAEKFKVLASNRTHQDQPKCGPNSHCCEMDCEVNNEILLCVLIDDGGFLVLSNQNHQ 900
Db      841  |||||leawaekfkvlasnrtthqdqpkcgpnshcemdcevnneillcvliddggflvlsnqnqh 900
Qy      901  WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF 960
Db      901  |||||wdqvgrffsevdanlmlalynnsfytrkesydyqaacapqppgnlgaaprgvfvptvadf 960
Qy      961  LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAEGLPETRESSCVMKQTQYYFGSVNA 1020
Db      961  |||||lnlawwtsaaawslfqqllygliyhswfqadpaeaeqlpetresscvmkqtqyyfgsvna 1020
Qy      1021 SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL 1080
Db      1021 |||||synaiidcgncsrlfhaqrlnntnllfvvaeplcsqceagrllqkethcpadgpeqcel 1080
Qy      1081 VQRPRYRRGPHICFDYNATEDTSDCGRGASFPPLSLGLVLSLQLLLLLGLPPRPQPQVLVH 1140
Db      1081 |||||vqrpryrrgphicfdynatedtsdcgrgasfpplslglvslqlllllglpprpqpqlvh 1140
Qy      1141 ASRRL 1145
Db      1141 |||||asrrl 1145

```

RESULT 2  
 R71015  
 ID R71015 standard; Protein; 1084 AA.





Qy 224 ELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW----RAPKKIDLYDVRRR 279  
 ||||| ||: || :|| :||:|||||:||||:| | |||||  
 Db 182 elnwtasaldevfkknreedpsllwqvfgsatglaryypaspwvdsrtpnkidlydvrrr 241

Qy 280 PWYIQGASSPKDMVIIVDVSGSVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPV 339  
 |||||:||||:|:|||||:||||:| | ||:||||:||||| || |  
 Db 242 pwyiqgaaspkdmlilvdvsgsvsgltlklirtsvsemletlsdddfvnvasfnsnaqdv 301

Qy 340 SCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMF 399  
 ||| ||||| ||:| : || | || || :||:| | | :||||:|:|  
 Db 302 scfqhlvqanvrnkkvldavnnitakgitdykkgfsafeqllynvnsrancnkiimlf 361

Qy 400 TDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIR 459  
 ||||:| |:| || :| ||| |||||: |:||| ||||:|||||  
 Db 362 tdggeeraqeifnkyn-kdkkvrfrfsvgqhnyergpiqwmacenkggyyeipsigair 420

Qy 460 INTQEYLDVLGRPMVLGKEAKQVQWNTVYEDALGLGLVVTGTLPVFNLTQ--DGPGEKK 517  
 |||||:||||| ||| ||||:|||||:| : |  
 Db 421 intqeyldvlgrpmvlagdkakqvqwnvldalelglvitgtlpvfnitgqfenktnlk 480

Qy 518 NQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKPQTTFREPVTL 577  
 |||||:| |:| ||||| :|| ||| ||||| |||||:| : |||||  
 Db 481 nqlilgvmgvdvsledikrltprftlcpngyyfaidpngyvllhpnlpknkpsqepvtl 540

Qy 578 DFLDAELEDENKEEIRRSIDGNKGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSL 637  
 |||||:| | ||| ||| ||||| |||||: | ||| |: |:|||  
 Db 541 dfldaelendikveirnkmidgesgektfrtlvksqderyidkgnrtytwtvpvngtdysl 600

Qy 638 GLVLPPYSTFYLQANLSDQILQVYFEFLPSSFESEGHVFIAPREYCKDLNASDNNTF 697  
 |||| || :||:| | : | | :| | | :|| | : ||||:|||| |||||  
 Db 601 alvlptysfyyikakleetitqarysetlcpdnfeesgytffiaprdocndlkisdnntef 660

Qy 698 LKNFIELMEKVTPDSKQCNNFLHNLILDTGITQQLVERVWRDQDLNTYSLAVFAATDG 757  
 | || | :|| :||: || | :|| :||| | | :||: | | | : | | |||  
 Db 661 llfnfefdrtktpnpscnadlinrvlldagftnelvqnywskqk-nikgvkarfvvtdg 719

Qy 758 GITRVFPNKAEDWTENPEPFNASFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILV 817  
 ||||:| :| |:| |||| : |||:|||| ||| |: : | |: ||:|  
 Db 720 gitrvypkeagenwqenpetyedsfykrslndnyvftapyfkn-sgpgayes---gimv 775

Qy 818 STAVELSLGRRTLRAVVGKLDLEAWAEKFKVLASNRTHQDQPQKC-GPNSHCEMDCEV 876  
 | |||: : : |:|||||:|: :| | | :| | | || |||  
 Db 776 skaveiyiqgkllkpavvgikidvnswiefnf----tktsirdp--cagp----vcdckr 824

Qy 877 NNEDLLCVLIDDGGFLVLSNQNHQWDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAA 936  
 |: : ||:|||||:| : :|:|||| |:| :|| | | | :||||:  
 Db 825 nsdvmdcvliddggfllmanhddytnqigrffgeidpslmrhlvnisvyafnkisydyqsv 884

Qy 937 CAPQPPGNLGAAPRGVFPVTVADFLNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAE 996  
 | | || | :||:|||| | : || :||||: || | | : | | :  
 Db 885 cepgaapkqgaghrsayvpsvadilqigwwataaawsilqqflsltfprlleavemedd 944

Qy 997 G-SPETRESSCVMKQTQYYFGSVNASYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLC 1055  
 : : ||: ||||:| : :|: :|||||:| :| ||||:|:|  
 Db 945 dftaslskqsciteqtqyffnddsksfsgvldcgncsrifhgeklmtnlifimveskgt 1004

Qy 1056 SQCEAGRLLQKETHCPADGPEQCELVQRPRYRRGPHICFDYNATEDTSDCGRGASFPPSL 1115  
 |: |:| | :||| |:|:||||:| | || | || :||| : |||  
 Db 1005 cpcdtrlliaeq--tsdgpnpcdmvqpryrkgpdvcfdnnvledytdcggvsglnpsl 1062

Qy 1116 GVLVSLQLLLL 1126  
 : : |:| |||  
 Db 1063 wyiigiqfl11 1073

RESULT 3  
 W63155  
 ID W63155 standard; Protein; 1084 AA.  
 XX  
 AC W63155;



Qy 224 ELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW----RAPKKIDLYDVRRR 279  
 ||||| ||: || :|| :||:|||||||: ||||:| | | |||||  
 Db 182 elnwtasaldevfkknreedpsllwqvfsgsatglaryypaspwvdsrtpnkidlydvrrr 241  
 Qy 280 PWYIQGASSPKDMVIIVDVSGSVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPV 339  
 |||||:||||:|:|||||||:|||| ||:||||:|||| | | |  
 Db 242 pwyiqgaaspkdmllilvdvsgsvsghltklirtsvsemletlsdddfvnvasfnsnaqdv 301  
 Qy 340 SCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMF 399  
 ||| ||||| ||:| : || | || | :||:| | | :|||:|:|  
 Db 302 scfqhlvqanvrnkkvldavnnitakgitdykkgfsafeqllynvnsrancnkiimlf 361  
 Qy 400 TDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNVDVTPQWMACANKGYFEIPSIGAIR 459  
 ||||:| |:| || :| || |||||: |:||| ||||:|||||  
 Db 362 tdggeeraqeifnkyn-kdkkvrfrfsvqghnyergpiqwmacenkggyyeipsigair 420  
 Qy 460 INTQEYLDVLGRPMVLGKEAKQVQWNTVYEDALGLGLVVTGTLPVFNLTQ--DGPGEKK 517  
 ||||| ||||| ||:| ||||| ||| ||||:|||||:| : |  
 Db 421 intqeyldvlgrpmvlagdkakqvqwnvylalelglvitgtlpvfnitgqfenktnlk 480  
 Qy 518 NQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKPQTTFREPVT 577  
 |||||:|:| ||||| :|| ||| |||| |||||:| : |||||  
 Db 481 nqlilgvmgvdvsledikrltpftlcpngyyfaidpnyvllhpnlpkpnkpsqepvtl 540  
 Qy 578 DFLDAELEDENKEEIRSMIDGNKGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSL 637  
 |||||:|:| ||| |||| | | ||||| |||||: | ||| |: |:|||  
 Db 541 dfldaelendikveirnkmdigesgektfrtlvksqderidkgnrtytwtvpvngtdysl 600  
 Qy 638 GLVLPPYSTFYQLQANLSDQILQVKYFEFLPSSFESEGHVFIAPREYCKDLNASDNTEF 697  
 |||| || :|:| | : | | :| | | :| | | :| ||||:| || |||||  
 Db 601 alvlptysfyyikakleetitqarysetlcpdnfeesgytffiaprdocndlkisdnntef 660  
 Qy 698 LKNFIELMEKVTPDSKQCNNFLHNLILDTGITQQLVERVWRDQDLNTYSLAVFAATDG 757  
 | || | :|: ||: || :|: || | | :||: | | | : | | |||  
 Db 661 llfnfidrktppnpscnadlinrvlldagftnelvqnywskqk-nikgvkarfvvtdg 719  
 Qy 758 GITRVFPNKAEDWTENPEPFNASFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILV 817  
 ||||:| :| |:| |||| : |||:|||| ||| |: : | |: ||:|  
 Db 720 gitrvypkeagenwqenpetyedsfykrslndndnyvftapyfkn-sgpgayes---gimv 775  
 Qy 818 STAVELSLGRRTLRLPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-GPNSHCEMDCEV 876  
 | |||: : : |:|||||:|:|: || | :| | | || |||  
 Db 776 skaveiyiqgkllkpavvgikidvnswienf-----tktsirdp--cagp---vcdckr 824  
 Qy 877 NNEDLLCVLIDDGGFLVLSNQNHQWDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAA 936  
 |:| : ||:|||||:|:| : |:|||| |:| :|| | | | :||||:  
 Db 825 nsdvmdcvilddggfllmanhddytngigrffgeidpslmrhlvnisvyafnksydyqsv 884  
 Qy 937 CAPQPPGNLGAAPRGVFPVTVADFLNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAE 996  
 | | || | :||:| | : || :||||: || | | : :| | :  
 Db 885 cepgaapkqgaghrsavpsvadilqigwwataaawsilqqflsltfprlleavemedd 944  
 Qy 997 G-SPETRESSCVMKQTQYYFGSVNASYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLC 1055  
 : : ||: ||||:| : : |:| :|||||:| :| ||||:|:|  
 Db 945 dftaslskqsciteqtqyffndsksfsgvldcgncsrifhgeklmtnlifimveskgt 1004  
 Qy 1056 SQCEAGRLLQKETHCPADGPEQCELVQRPRYRRGPHICFDYNATEDTSDCGRGASFPFSL 1115  
 |: | |:| | :|| | |:|:|:||||:| | || | || :||| : |||  
 Db 1005 cpcdtrlliqaeq--tsdgpnpdmvqkpryrkgpdcfdnnvledytdcggvsglnpsl 1062  
 Qy 1116 GVLVSLQLLLL 1126  
 : : | |||  
 Db 1063 wyiigiqflll 1073

RESULT 11  
 R73056  
 ID R73056 standard; Protein; 1106 AA.  
 XX

AC R73056;  
 XX  
 DT 02-NOV-1995 (first entry)  
 XX  
 DE Rabbit skeletal calcium channel (alpha)2-subunit.  
 XX  
 KW Calcium channel; (alpha)2 subunit.  
 XX  
 OS Oryctolagus cuniculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /label= signal peptide  
 FT Modified-site 94  
 FT /label= potential N-linked glycosylation site  
 FT Modified-site 138  
 FT /label= see above  
 FT Modified-site 186  
 FT /label= see above  
 FT Modified-site 326  
 FT /label= see above  
 FT Modified-site 350  
 FT /label= see above  
 FT Modified-site 470  
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 FT Modified-site 606  
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 FT Modified-site 697  
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 FT /label= see above  
 FT Modified-site 988  
 FT /label= see above  
 FT Modified-site 1081  
 FT /label= see above  
 FT Modified-site 503  
 FT /label= potential cAMP-dependent phosphorylation  
 FT Modified-site 848  
 FT /label= see above  
 FT Region 448..471  
 FT /label= putative transmembrane region  
 FT Region 921..945  
 FT /label= see above  
 FT Region 1082..1101  
 FT /label= see above  
 XX  
 PN US5407820-A.  
 XX  
 PD 18-APR-1995.  
 XX  
 PF 04-APR-1988; 88US-0176899.  
 XX  
 PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1988; 88US-0176899.  
 PR 13-JUL-1992; 92US-0914231.  
 XX  
 PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 XX  
 PI Brenner R, Ellis SB, Harpold MM, Schwartz A, Williams ME;



XX  
 DR WPI; 1995-161088/21.  
 DR N-PSDB; Q87979.  
 XX  
 PT DNA encoding alpha-1 and alpha-2 calcium channel sub-unit(s) -  
 PT for detecting calcium channel agonists/antagonists or  
 PT Lambert-Eaton syndrome.  
 XX  
 PS Disclosure; Fig 2; 32pp; English.  
 XX  
 CC The nt sequence in Q87979 was determined from two clones which  
 CC overlapped to span the coding sequence of the (alpha)2-subunit.  
 CC Five nt differences (see Q87979 FT) among individual clones were  
 CC observed resulting in four AA changes. The AAs were finally  
 CC determined to be as follows: Asn at residue 57, Lys at residue 116  
 CC and a deletion of Ser at residue 620. The deduced AA sequence  
 CC (R73056) yields a calculate Mr of 125,018, in contrast to the  
 CC observed Mr 165K-175K (under non-reducing conditions; Mr 135K-  
 CC 175K under reducing conditions) determined previously using SDS  
 CC polyacrylamide gel electrophoresis.  
 XX  
 SQ Sequence 1106 AA;

Query Match 49.9%; Score 3040; DB 16; Length 1106;  
 Best Local Similarity 53.0%; Pred. No. 9.1e-259;  
 Matches 595; Conservative 183; Mismatches 276; Indels 68; Gaps 20;

Qy 42 RPL-----WLLLPLLPLLAAPGASAYSFPQQHTMQHWARRLEQEV DGV MRIFGGVQ 92  
 ||| || :| | :| || |:: | ::::: : : ||  
 Db 5 rplawtltlwqawl-----iligp-sseepfpsavtikswvdkmqedlvtlaktasgvh 57

Qy 93 QLREIYKDNRNLFVQENEPQKLVEKVAGDIESLLDRKVQALKRLADAAENFQKAHRWQD 152  
 || :||: ::|: |: | :||| | ||| || : :|| ||| || | ||:|::  
 Db 58 qlvdiyekyqdltyvepnnarqlveiaardieklslsrskalvrlaleaekvqaahqwre 117

Qy 153 NIKEEDIVYYDAKADAELDDPESEDVERGSKASTLRDLDFIEDPNFKNKVNYSYAAVQIPT 212  
 : :|||:| | || | | ||: : : ||:| ||: |:| :||| |||  
 Db 118 dfasnevyynakddl---dpekndsepgsq--rikpvfiddanfrqvsvyqhaavhipt 172

Qy 213 DIYKGSTVILNELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW----RAP 268  
 |||:| |:| |:| ||| |||:| |:| :| |:| |:| |:| |:| |:| |:| |:| |:|  
 Db 173 diyegstivlnelnwtsalddvfkknreedpsllwqvfgsatglaryypaspwvdsrtp 232

Qy 269 KKIDLYDVRRRPWYIQGASSPKDMVIIVDVSGSVSGLTLKLMKTSVCEMLDLSDDDYVN 328  
 ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|  
 Db 233 nkidlydvrrrpwyiggaaspkdmllilvdvsgsvsgltklirtsvsemletlsdddfvn 292

Qy 329 VASFNEKAQPVSCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNIT 388  
 |||| | | ||| ||||| |:| : || | | | |:|:| | |:|  
 Db 293 vasfnsnaqdvscfqlvqanvrnkkvdkavnnitakgitdykkqfsfafeqllnynvs 352

Qy 389 RANCNKIMMFTDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNYDVTPLQWMACANKGY 448  
 ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|  
 Db 353 rancnkiimlftdggeeraqeifakyn-kdkkvrvtftsvgqhnydrqpiqwmacenkg 411

Qy 449 YFEIPSIGAIRINTQEYLDVLRPMVLGKEAKQVQWTVNYEDALGLGLVVTGTLPVFN 508  
 |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|  
 Db 412 yyeipsigairintqeyldvlgprmvlagdkakqvqwtvnyldalelglvitgtlpvfni 471

Qy 509 TQ--DGPGEKKNQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKP 566  
 | : ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|  
 Db 472 tgqfenktnlknqlilgvmgvdvsledikrltprftlcpngyyfaidpngyvllhpnlp 531

Qy 567 Q-----TTNFR-----EPVTLDFLDAELEDENKEEIRRS MIDGNKGHKQIR 607  
 : | | | ||||| |:| | ||| ||| | | |  
 Db 532 kpigvgiptinlrkrrpnvqnpksqepvtldfldaelendikveirnkmidgesgektfr 591

Qy 608 TLVKS LDERYIDEVTRNYTWVPIRSTNY-SLGLVLPYSTFY LQANLSDQILQVKYFEFL 666  
 |||| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|  
 Db 592 tlvksqderidkgnrtytwtvpngtdysslalvltysfyyikakieetitqarysetl 651

Qy 667 LPSSFESEGHVFIAPREYCKDLNASDNNTEFLKNFIELMEKVT PDSKQCNNFLLHNLILD 726  
 | :|| |: |:| |:| || ||||| || | ::| ::| || |:| ::||  
 Db 652 kpdnfeesgytflaqrDYCSdlkpsdnntefllnfnefidrkt pnnqscntdlinrvlld 711

Qy 727 TGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNASFYRRS 786  
 | | :||: | | | : | | ||||| :| :| |:| ||| : |||:|  
 Db 712 agftnelvqnywskqk-nikgvkarfvvtdggitr vypkeagenwqenpetyedsfykrs 770

Qy 787 LDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTL RPAVVGKLDLEAWAE 846  
 ||| ||| |: : | |: ||:| |||: : : |:| |||:|:|: :| |  
 Db 771 ldndnyvftapyfnk-sgpgayes---gimvskaveiyiqgkllkpavvgikidvnswie 826

Qy 847 KFKVLASNRTHQDQPQKC-GPNSHCEMDCEVNNE DLLCVLIDDGGFLVLSNQNHQWDQVG 905  
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 Db 827 nf-----tktsirdp--cagp----vcdckrnsdvmdcvilddggfllmanhddytnqig 875

Qy 906 RFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVPTVADFLNLAW 965  
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 Db 876 rffgeidpslmrhlvnisvyafnksydyqsvcepgaapkqgaghrs ayvpsiadilqigw 935

Qy 966 WTSAAAWSLFQQLLYGLIYHSWFQ-ADPAEAE GSPETRESSCVMKQTQYYFGSVNASYNA 1024  
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 Db 936 wataaawsilqqfllsltfprlleadmedddftasmskqsciteqtqyffdnksksfsg 995

Qy 1025 IIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCELVQRP 1084  
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Qy 1085 RYRRGPHICFDYNATEDTSDCGRGASFPPSLGVLVSLQLLLL 1126  
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 Db 1054 ryrkgpdcvcdnnvledytdcggvsglnpslwsiiqiqfvll 1095

RESULT 15  
 W37879  
 ID W37879 standard; Protein; 1091 AA.  
 XX  
 AC W37879;  
 XX  
 DT 28-AUG-1998 (first entry)  
 XX  
 DE Human calcium channel a2d subunit.  
 XX  
 KW Calcium channel; human; central nervous system disorder;  
 KW Lambert-Eaton syndrome; diagnosis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9811131-A2.  
 XX  
 PD 19-MAR-1998.  
 XX  
 PF 11-SEP-1997; 97WO-US16146.  
 XX  
 PR 16-SEP-1996; 96US-0713118.  
 XX  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 XX  
 PI Chen ARS, Franco R, Shuey DJ;  
 XX  
 DR WPI; 1998-207325/18.  
 DR N-PSDB; V29060.  
 XX  
 PT DNA encoding human neuronal calcium channel subunit(s) - useful for  
 PT diagnosis of and treatment of central nervous system disorders, e.g.  
 PT Lambert-Eaton syndrome

```

XX
PS   Disclosure; Fig 2; 89pp; English.
XX
CC   This polypeptide comprises the a2d subunit of the human neuronal
CC   calcium channel. cDNA clones (see V29059-61) encoding the a1B
CC   subunit (see W37878), the a2d subunit and a b3 subunit (see W37880)
CC   have been isolated. These have been inserted into expression
CC   vectors and are stably expressed in transformed cell lines. The
CC   transformed cells show omega-conotoxin GVIA binding activity,
CC   and omega-conotoxin GVIA toxin sensitive potassium-stimulated
CC   calcium upstroke, indicating that the proteins expressed by the
CC   clones are capable of forming a functioning calcium channel.
CC   Nucleic acids encoding the 3 subunits, as well as vectors, host
CC   cells and methods of isolating nucleic acids encoding related
CC   calcium channels are disclosed. Fusion proteins incorporating the
CC   subunit proteins, antibodies, and assays for identifying agents
CC   that modulate calcium channel activity are also provided. Such
CC   agents can be used to treat certain central nervous system
CC   disorders by altering calcium channel activity. Methods of
CC   diagnosing diseases associated with particular calcium channels,
CC   such as Lambert-Eaton syndrome, are disclosed.
XX
SQ   Sequence   1091 AA;

Query Match          49.8%; Score 3030.5; DB 19; Length 1091;
Best Local Similarity 53.8%; Pred. No. 6.1e-258;
Matches 591; Conservative 175; Mismatches 293; Indels 39; Gaps 15;

Qy   44 LWLLLPLLPLLAAPGASAYSFPQOHTMQHWARRLEQEV DGV MRIFGGVQQLREIYKDNRN 103
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Db   7 laltltlftqsligpsseepfpsavtikswvdkmqedlvtlaktasgvnqlvdiyekyqd 66

Qy  104 LFEVQENEPQKLVEKVAGDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYD 163
      | : | : | : | | | | | : | | | | | | | : | : | : | : | : | :
Db  67 lytvepnarqlveiaardiekllsnrskalvslaleakvqaahqwredfasnevyyn 126

Qy  164 AKADAELDDPESEDVERGSKASTLR LDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILN 223
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Db  127 akddl--dpekndsepgsq--rikpvfiedanfgrqisyqhaavhiptdiyegstivln 181

Qy  224 ELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW----RAPKKIDLYDVRRR 279
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Db  182 elnwtsaldevfknreedpsllwqvfgsatglaryypaspwvdsrtpnkidlydvrrr 241

Qy  280 PWYIQGASSPKDMVIIVDVSGSVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPV 339
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Db  242 pwyiqgaaspkdmlilvdvsgsvsgltlklirtsvsemletlsdddfvnvasfnsnaqdv 301

Qy  340 SCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMF 399
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Db  302 scfqhlvqanvrnkkvldavnnitakgitdykkgfsfafaqllnynvsrancnkiimlf 361

Qy  400 TDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNVDVTP LQWMACANKGYFFEIP SIGAIR 459
      | | | | : | : | | : : | | | | | : | : | | | | | : | | | |
Db  362 tdggeeraqeifnkyn-kdkkvrvfrfsvgqhnyergpiqwmacenkgyyeipsigair 420

Qy  460 INTQEYLDVLRPMVLGKKEAKQVQWNTNVEYEDALGLGLVVTGTLPVFNLTQ--DGPGEKK 517
      | | | | | | | | | | : | | | | | | | | | : | : | | | : | : |
Db  421 intqeyldvlgrpmvlagdkakqvqwtvnyldalelglvitgtlpvfnitgqfenktnlk 480

Qy  518 NQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKPQTTFREPVTL 577
      | | | | | : | : | | | | : | | | | | | | | | : | : | | |
Db  481 nqlilgvmgvdvsledikrltprftlcpngyyfaidpnygallhpnlpknpksqepvtl 540

Qy  578 DFLDAELEDENKEEIRRSMDGNKGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSL 637
      | | | | | : | | | | | | | | | | | : | | | | : | : | |
Db  541 dfldaelendikveirnkmidgesgektfrtlvksqderyidkgnrtytwtvpvngtdysl 600

Qy  638 GLVLPPYSTFY LQANLSDQILQ-----VKYFEFLPSSFESEGHVFIAPREYCKDLNA 690
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Db 601 alvlptysfyyikakleetitqarskkkgmkmdsetlkpdnfeesgytftiaprdocndlki 660  
 Qy 691 SDNNTFLKNFIELMEKVTPDSKQCNNFLHNLILDGTGITQLVERVWRDQDLNTYSLLA 750  
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 Db 661 sdnntefllnfnefidrktpnnpnscadlinrvlldagftnelvqnywskqk-nikgvka 719  
 Qy 751 VFAATDGGITRVFPNKAEDWTENPEPFNASFYRRSLDNHGYVFKPPHQDALLRPLELEN 810  
 | |||||:| :| |:| ||| : ||:|||| | | |: : | | :  
 Db 720 rfvtddggitrvypkeagenwqenpetyedsfykrslndndnyvftapyfkn-sgpgayes 778  
 Qy 811 DTVGILVSTAVELSLGRRTLRAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-GPNSH 869  
 ||:| |||: : : |:| |||: |:| :| | | :| | | |  
 Db 779 ---gimvskaveiyiqgkllkpavvgikidvnswienf-----tktsirdp--cagp--- 825  
 Qy 870 CEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQWDQVGRFFSEVDANLMLALYNNSFYTRKE 929  
 ||: |: : ||:|||||:| : : |:| ||| |:| :| | | | :  
 Db 826 -vcdckrnsdvmdevildddggfllmanhddytnqigrffgeidpslmrhlvnisvyafnk 884  
 Qy 930 SYDYQAACAPQPPGNLGAAPRGVFPVTVADFLNLAWWTSAAAWSLFQQLLYGLIYHSWFQ 989  
 ||||: | | | | :|:| | | : | | :|||: | | | : :  
 Db 885 sydyqsvcepgaapkqgaghrsavpsvadilqigwwataaawsilqqfllsltfprlle 944  
 Qy 990 ADPAEAEAG-SPETRESSCVMKQTQYYFGSVNASYNAIIDCGNCSRLFHAQRLTNTNLLFV 1048  
 | | : : : ||: :|||:| : : |: :||| |||:| | :| |||:| :  
 Db 945 avemedddftaslskqsciteqtqyffndsksfsgvldcgncsrifhgeklmntnlifi 1004  
 Qy 1049 VAEKPLCSQCEAGRLLQKETHCPADGPEQCELVQRPRYRRGPHICFDYNATEDTSDCGRG 1108  
 : | | : | | : || | :|:| |||:| | :| | | | :||  
 Db 1005 mveskgtpcdtrlliaeq--tsdgpnpdmvkgpryrkgpdvcfdnnvledytdcggv 1062  
 Qy 1109 ASFPPSLGVLVSLQLLLL 1126  
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 Db 1063 sglnpnlwyiigiqflll 1080

RESULT 2

US-08-223-305C-56

; Sequence 56, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223,305C

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1084 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-56

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Query Match          50.2%; Score 3054; DB 2; Length 1084;
Best Local Similarity 54.3%; Pred. No. 3.4e-265;
Matches 592; Conservative 175; Mismatches 292; Indels 32; Gaps 14;

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Qy   44 LWLLPLLLPLLAAPGASAYSFPQQHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRN 103
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Qy  104 LFEVQENEPQKLVEKVAGDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYD 163
    | : | : | : | | | | | : : | | | | | : | | : : | | :
Db  67  LYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASNEVVYYN 126

Qy  164 AKADAELDDPESEDVERGSKASTLRDLFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILN 223
    | | | | | | | | | | | : : : | | | | | : : | : | | | | | : | |
Db  127 AKDDL---DPEKNDSEPGSQ--RIKPVFIEDANFGRQISYQHAAVHIPTDIYEGSTIVLN 181

Qy  224 ELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW----RAPKKIDLYDVRRR 279
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Db  182 ELNWTALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVRRR 241

Qy  280 PWYIQGASSPKDMVIVDVSGSVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPV 339
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Qy  400 TDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNVDVTPQWMACANKGYFFEIPSIGAIR 459
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Db  362 TDGGEERAQEIFNKYN-KDKKVRVFRFSVGQHNVERGPQWMACENKGYFFEIPSIGAIR 420

Qy  460 INTQEYLDVLGRPMVLGKQVQWNTVYEDALGLGLVVTGTLVPVFNLTQ--DGPGEKK 517
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Db  421 INTQEYLDVLGRPMVLGDKAKQVQWNTVYLDALGLGLVITGTLVPVFNITGFENKTNLK 480

Qy  518 NQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKPQTTFNREPRTL 577
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Db 481 NQLILGVMGVDVSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540

Qy 578 DFLDAELEDENKEEIRSMIDGNKGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSL 637  
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Db 541 DFLDAELENDIKVEIRNMIDGESGEKTFRTL VKSQDERYIDKGNRTYTWTVPVNGTDYSL 600

Qy 638 GLVLPPYSTFYLQANLSDQILQVKYFEFLPSSFESEGHVFIAPREYCKDLNASDNNTEF 697  
 |||| | :|::| | : | | :| | | :|| |: ||||:| | | |||||

Db 601 ALVLPTYSFYYIKAKLEETITQARYSETLKPDNFEESGYTFIAPRDYCNLDKISDNNTEF 660

Qy 698 LKNFIELMEKVTPDSKQCNNFLLHNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDG 757  
 | || | ::| ||:: || }:: ::|| | | :||: | | | : | | |||

Db 661 LLNFNEFIDRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQK-NIKGVKARFVVTGD 719

Qy 758 GITRVFPNKAEDWTENPEPFNASFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILV 817  
 ||||:| :| |:| |||| : |||:|||| ||| |: : | |: |||

Db 720 GITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNK-SGPGAYES---GIMV 775

Qy 818 STAVELSLGRRTLPAVVGKLDLEAWAEKFKVLASNRTHQDQPQKC-GPNSHCEMDCEV 876  
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Db 776 SKAVEIYIQGKLLKPAVVGKIDVNSWIENF-----TKTSIRDP--CAGP----VCDCKR 824

Qy 877 NNEDLLCVLIDDGGFLVLSNQNHQWDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAA 936  
 |:: : ||::|||||:::| : :|:|||| |::| | | | | | | | | | | |

Db 825 NSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSYDYQSV 884

Qy 937 CAPQPPGNLGAAPRGVFPVPTVADFLNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAE 996  
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Db 885 CEPGAAPKQGAGHRSAVPSVADILQIGWWATAAAWSILQQFLLSLTFPRLLEAVEMEDD 944

Qy 997 G-SPETRESSCVMKQTQYYFGSVNASYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLC 1055  
 : : ||: ||||:| : : |: : |||||:| | :| ||||:|: |

Db 945 DFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCSRIFHGEKLMNTNLIFIMVESKGT 1004

Qy 1056 SQCEAGRLLQKETHCPADGPEQCELVQRPRYRRGPHICFDYNATEDTSDCGRGASFPFSL 1115  
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Db 1005 CPCDTRLLIQAEQ--TSDGPNPCDMVKQPRYRKGPDVCFDNNVLEDYTDGCGVSGLNPSL 1062

Qy 1116 GVLVSLQLLLL 1126  
 :: :| |||

Db 1063 WYIIGIQFLLL 1073

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2001, 13:19:43 ; Search time 392.32 Seconds  
 (without alignments)  
 426.713 Million cell updates/sec

Title: US-09-397-550-20  
 Perfect score: 6089  
 Sequence: 1 MAVPARTCGASRPGPARTAR.....LLGLPPRPQPQVLVHASRRL 1145

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 901707 seqs, 146207799 residues

Total number of hits satisfying chosen parameters: 901707

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries